



## SEQUENCE LISTING

RECEIVED  
AUG 28 2002  
TECH CENTER 1600/2900

<110> Prayaga, Suhhirdas K  
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

<400> 1

accaatggtc tccttgctgg tggcattggt gatgatctcc tgccacatct attccctttt 60  
ctgcgacctg cctaaagctc aggtgatctc tgccctccat aagatgcacc agcagatctt 120  
cagcctcttt ttacacaagg gcttgctctga tgcttggaat agggccttcc tggacaaact 180  
ccagactgga ttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240  
gaagcaagag tctgccctgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300  
gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgctcg 360  
aatggtaaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420  
gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaag agctg 475

<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Ser Leu Leu Val Ala Leu Val Met Ile Ser Cys His Ile Tyr  
1 5 10 15

Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His  
20 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser  
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His  
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

65 70 75 80

Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg  
85 90 95

Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn  
100 105 110

Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr  
115 120 125

Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn  
130 135 140

Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu  
145 150

<210> 3  
<211> 610  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (74)..(208)  
<223> Wherein n is a or t or c or g.

<400> 3  
accaatggtc tccttgctgg tggcattggt gatgatctcc tgccacatct attccctttt 60  
ctgcgacctg cctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120  
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180  
nnnnnnnnnn nnnnnnnnnn nnnnnnnnaa agctcagggtg atttctgccc tccataagat 240  
gcaccagcag atcttcagcc tctttttaca caaggccttg tctgatgctt ggaatagggc 300  
cttcctggag aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360  
tggtatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420  
aaagaggtac ttccaggagg tacatttctt cttgaaagag aggaaattca ggaactgtac 480  
ctgggagggt gtcgtaatgg taaagggtt tttcttaagc acaaaacttc aagaaaaaga 540  
gaacagaaga aaagagaact gcaaaaaaaa tctggaaaag gtaatctatt tagcagaaga 600  
gtgaaagctg 610

<210> 4  
<211> 199  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (24)..(68)  
<223> Wherein Xaa is any amino acid.

<400> 4  
Met Val Ser Leu Leu Val Ala Leu Val Met Ile Ser Cys His Ile Tyr  
1 5 10 15  
Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His  
65 70 75 80

Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp  
85 90 95

Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu  
100 105 110

Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser  
115 120 125

Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln  
130 135 140

Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp  
145 150 155 160

Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln  
165 170 175

Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys  
180 185 190

Val Ile Tyr Leu Ala Glu Glu  
195

<210> 5  
<211> 1887  
<212> DNA  
<213> Homo sapiens

<400> 5  
atggccatcc tcccgttgct cctgtgcctg ctgccgctgg cccctgcctc atccccaccc 60  
cagtcagcca caccagccc atgtcccgc cgctgccgt gccagacaca gtcgctgccc 120  
ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccc 180  
gcagccgagc tgcggctggc agacaacttc atgcctccg tgcgcgccc cgacctggcc 240  
aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300  
ggcgcccttc cgcacctgcg ggccttgcgt gccctgcacc tggatggcaa ccggctgacc 360  
tactgggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420  
aaccagctgg cagcgttggc ggcggcgcc ctggatgatt gtgcccagac actggaggac 480  
ctcgacctct cctacaacaa cctcagacag ctgccctggg aggccttggg ccgcctgggg 540  
aacgtcaaca cgttgggcct cgaccacaac ctgctggcct ctgtgcccgc cggcgctttt 600  
tcccgcctgc acaagctggc ccggtggac atgacctcca accgctgac cacaatcca 660  
cccgacccac tcttctcccg cctgcccctg ctgcgcaggc cccgggctc gccgcctct 720  
gccctggtgc tggccttttg cggaacccc ctgcactgca actgcgagct ggtgtggctg 780  
cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt cccacctgc tctgggcggc 840  
cgctacttct gggcggtggg cgaggaggag tttgtctgag agccgcccgt ggtgactcac 900

cgctcaccac ctctggctgt gcccgaggt cgcccggtg ccttgcgtg ccgggcagt 960  
 ggggacccag agccccgtgt gcgttgggtg tcacccagagg gccggctgct aggcaactca 1020  
 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080  
 ggtggcaact tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140  
 ctgactgtgg gtccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200  
 cgggacgggg atcctgatgc tctcaccaca ccctccgctg cctctgcttc tgccaagggtg 1260  
 gccgacactg ggccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320  
 gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380  
 tacaacagct cggctgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440  
 ttcctgctga cggacctggc gtcaggcccg acctacgata tgtgcgtgct cgccgtgtat 1500  
 gaggacagcg ccacgggggt cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560  
 gaacctgctg tgcggccatg cggggcgccg cacgctccct tcctgggcgg cacgatgata 1620  
 atcgcgctgg gcggggtcat cgtagcctcg gtactggtct tcactcttct gctgctaata 1680  
 cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740  
 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgc 1800  
 ccggagcccc cggcgctcag ggccccacac gtggtccagc tggactgcga gccctggggg 1860  
 cccggccacg aacctgtggg accctag 1887

<210> 6  
 <211> 628  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ala Ile Leu Pro Leu Leu Leu Cys Leu Leu Pro Leu Ala Pro Ala  
 1 5 10 15  
 Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys  
 20 25 30  
 Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala  
 35 40 45  
 Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu  
 50 55 60  
 Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala  
 65 70 75 80  
 Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg  
 85 90 95  
 His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu  
 100 105 110  
 His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg  
 115 120 125  
 Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala  
 130 135 140  
 Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp  
 145 150 155 160  
 Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu  
 165 170 175

Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu  
 180 185 190  
 Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg  
 195 200 205  
 Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu  
 210 215 220  
 Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser  
 225 230 235 240  
 Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu  
 245 250 255  
 Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys  
 260 265 270  
 Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu  
 275 280 285  
 Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro  
 290 295 300  
 Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val  
 305 310 315 320  
 Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu  
 325 330 335  
 Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu  
 340 345 350  
 Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala  
 355 360 365  
 Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly  
 370 375 380  
 Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro  
 385 390 395 400  
 Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala  
 405 410 415  
 Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln  
 420 425 430  
 Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Thr Pro Asp Gln  
 435 440 445  
 Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser  
 450 455 460  
 Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser  
 465 470 475 480

Sub  
 D5  
 Cont

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val  
 485 490 495  
 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro  
 500 505 510  
 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly  
 515 520 525  
 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly  
 530 535 540  
 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met  
 545 550 555 560  
 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro  
 565 570 575  
 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro  
 580 585 590  
 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala  
 595 600 605  
 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu  
 610 615 620  
 Pro Val Gly Pro  
 625

<210> 7  
 <211> 802  
 <212> DNA  
 <213> Equus caballus

<400> 7  
 aaatcagaga tattataagt acacatatcc ctatttaacgg cctagttggc aagaatgtca 60  
 tcagagaacc tcggtccaag ttcagagaca cccagctcag ccaggccagc agcaccctcg 120  
 ttttcccat ggccctcctg cctctctct tgcagccct ggtggtgtac gagttatggc 180  
 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctgggttagc aggaagaact 240  
 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300  
 acttcagggt cccccaggac atggcggatg gcaggcagtt cccagaggcc caggccgcgt 360  
 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420  
 ctgcctggaa cagcaccctc ctggacgaac tctgcacggg actccttcgg cagctggaag 480  
 acctggacac ctgtttggag caggagatgg gagaggaaga atctgccctg ggaactgtgc 540  
 gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600  
 aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660  
 cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720  
 attctcctta actactgggt catgttacc ttgcatatgt ccttggtcat ttcaaaaggc 780  
 tcttatttct gctttagtct ag 802

<210> 8  
 <211> 195  
 <212> PRT

<211> Homo sapiens

<400> 8

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr  
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
195

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser  
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu  
20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser  
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu  
 50 55 60  
 Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu  
 65 70 75 80  
 Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser  
 85 90 95  
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu  
 100 105 110  
 His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly  
 115 120 125  
 Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys  
 130 135 140  
 Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser  
 145 150 155 160  
 Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser  
 165 170 175  
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu  
 180 185 190  
 Gly Ser Pro  
 195

<210> 10  
 <211> 117  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:pfam00143  
 Domain 71-187

<400> 10  
 Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys  
 1 5 10 15  
 Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn  
 20 25 30  
 Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr  
 35 40 45  
 Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro  
 50 55 60  
 Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr  
 65 70 75 80



Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys  
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser  
100 105 110

Ser Thr Ala Leu Gln  
115

<210> 11  
<211> 194  
<212> PRT  
<213> Felis catus

<400> 11  
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val  
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp  
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu  
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met  
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser  
180 185 190

Glu Lys

<210> 12

<211> 195  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
1 5 10 15  
Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu  
20 25 30  
Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
35 40 45  
Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu  
50 55 60  
Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
65 70 75 80  
His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
85 90 95  
Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu  
100 105 110  
His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
115 120 125  
Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
130 135 140  
Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
145 150 155 160  
Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser  
165 170 175  
Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu  
180 185 190  
Ser Ser Pro  
195

<210> 13  
<211> 195  
<212> PRT  
<213> Equus caballus

<400> 13

Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu  
1 5 10 15  
Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu  
20 25 30

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser  
 35 40 45  
 Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp  
 50 55 60  
 Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu  
 65 70 75 80  
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
 85 90 95  
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu  
 100 105 110  
 Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly  
 115 120 125  
 Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys  
 130 135 140  
 Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser  
 145 150 155 160  
 Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser  
 165 170 175  
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu  
 180 185 190  
 Gly Ser Pro  
 195

<210> 14  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr  
 1 5 10 15  
 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
 20 25 30  
 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
 35 40 45  
 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
 50 55 60  
 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
 65 70 75 80  
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
 100 105 110  
 His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
 115 120 125  
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
 130 135 140  
 Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
 145 150 155 160  
 Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
 165 170 175  
 Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
 180 185 190  
 Gly Ser Ser  
 195

<210> 15  
 <211> 65  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Consensus  
 sequence

<400> 15  
 Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser  
 1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln  
 20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys  
 35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu  
 50 55 60

Gln  
 65

<210> 16  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
 1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
 20 25 30  
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
 35 40 45  
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
 50 55 60  
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
 65 70 75 80  
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
 85 90 95  
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
 100 105 110  
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
 115 120 125  
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
 130 135 140  
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu  
 145 150 155 160  
 Thr Gly Tyr Leu Arg Asn  
 165

<210> 17  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
 1 5 10 15  
 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
 20 25 30  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
 35 40 45  
 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
 50 55 60  
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
 65 70 75 80  
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
 85 90 95  
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

100 105 110  
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
 115 120 125  
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
 130 135 140  
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145 150 155 160  
 Leu Arg Ser Lys Glu  
 165  
 <210> 18  
 <211> 189  
 <212> PRT  
 <213> Mus musculus  
 <400> 18  
 Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr  
 1 5 10 15  
 Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu  
 20 25 30  
 Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser  
 35 40 45  
 Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu  
 50 55 60  
 Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu  
 65 70 75 80  
 Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser  
 85 90 95  
 Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu  
 100 105 110  
 His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly  
 115 120 125  
 Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg  
 130 135 140  
 Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser  
 145 150 155 160  
 Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser  
 165 170 175  
 Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys  
 180 185

full  
 cont  
 15

<210> 19  
<211> 195  
<212> PRT  
<213> Antilocapra americana

<400> 19

Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr  
1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro  
20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser  
35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu  
50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu  
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly  
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys  
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser  
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser  
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu  
180 185 190

Ala Ser Ser  
195

<210> 20  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala  
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile  
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val  
35 40

<210> 21

<211> 184

<212> PRT

<213> Equus caballus

<400> 21

Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys  
1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu  
20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu  
50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val  
65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser  
85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu  
100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly  
115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg  
130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser  
180

<210> 22

<211> 92

<212> PRT

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence:Consensus  
sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu  
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys  
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp  
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly  
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala  
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln  
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

gcctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg 60  
tctgaacttg aagacacccc acattccaag atgcccaggg ttcttgggaa tgcctggggg 120  
tcttcgatcc ggaaaatcct accggcatcc tcttagggag ggattattat tattattttt 180  
ctttaatctg gaagagaaga gaacaagtgt tgcttttccc cccttcttct tgctaaacgc 240  
catggatata actgaataag cggctcaggg dtttccccgc gtggacgtcc gaggccacca 300  
tctgcctgca ttgcgcggag ccgcccggag gtttagctcg agtctgtctc gggcggggaa 360  
ggatgcgtgg ccgagccggg gagcccgggc gccccgcgga gccggcctcg gtgccacca 420  
gccgggggta gatgtgctt cggccaggcg ctgagtacc agaccatgga gacctgctt 480  
pgtggcctgc tagcgttttg catggcgttt gccgtggtcg acgctgccc caagtactgt 540  
gtctgccaga atctgtctga gtcactgggg accctgtgcc cctccaaggg gctgctcttt 600  
gtacccccctg atattgaccg ggggacagtg gagctgcgcc tgggcccga cttcatcatc 660  
cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720  
aacaccatca gccacatcca gcccttttcc tttctggacc tcgagagcct ccgtccctg 780  
catcttgaca gcaatcggct gccaaagcctt ggggaggada ccctccgggg cctggtcaac 840  
ctgcagcacc ttatcgtgaa caacaaccag ctgggcccga tcgcagatga ggcttttgag 900  
gacttctctg tgacattgga ggatctggac ctctcctaca acaacctcca tggcctgccg 960  
tgggactccg tgcgacgcat ggtcaacctc caccagctga gcctggacca caacctgctg 1020  
gatcacatcg ccgagggcac ctttgacagac ctgcagaaac tggcccgcct ggatctcacc 1080  
tccaatcggc tgcagaagct gccccctgat cccatctttg ccgctccca ggcttcgggt 1140  
ttgacagcca caccctttgc cccacccttg tcttttagtt ttgggggtaa cccacttcac 1200  
tgcaattgtg agcttctctg gctgcggagg cctcagcggg acgatgacct ggaaacctgt 1260  
ggctccccag ggggcccctca gggctcgctac ttctggcatg tgcgtgagga ggagtttgtg 1320  
tgcgagccgc ctctcatcac ccagcacaca cacaagttgc tggttctgga gggccaggcg 1380  
gccacactca agtgcaaagc cattggggac cccagcccc ttatccactg ggtagcccc 1440  
gatgaccgcc tggtagggaa ctctcaagg accgctgtct atgacaatg caccctggac 1500  
atcttcatca ccacatctca ggacagtggg gccttcacct gcattgctc caatgctgcc 1560

gagaggcca cggccatggt ggaggtctcc atcgtccagc tgccacacct cagcaacagc 1620  
 accagccgca ctgcaccccc caagtcccg cctctcagaca tcactggctc cagcaagacc 1680  
 agcgggggag gtggaggcag tgggggcgga gagcctccca aaagcccccc ggaacgggct 1740  
 gtgcttgtgt ctgaagtgtac caccacctcg gccctgggtca agtgggtctgt cagcaagtca 1800  
 gcaccgagg tgaagatgta ccagctgcag tacaactgct ctgacgatga ggtactgatt 1860  
 tacaggatga tcccagcctc caacaaggcc ttcgtgggtca acaacctggt gtcagggact 1920  
 ggctacgact tgttgtgtgt ggccatgtgg gatgacacag ccacgacact cacggccacc 1980  
 aacatcgagg gctgcgcccc gttcttcacc aaggctgact acccgagtg ccagtccatg 2040  
 cacagccaga ttctgggagg caccatgatc ctggtcatcg ggggcatcat cgtggccacg 2100  
 ctgctgggtt tcatcgatcat cctcatgggt cgctacaagg tctgcaacca cgaggccccc 2160  
 agcaagatgg cagcgcccggt gagcaatgtg tactcgcaga ccaacggcgc ccagccaccg 2220  
 cctccaagca gcgcaccagc cggggccccc cgccagggcc cgccgaaggt ggtgggtgcgc 2280  
 aacgagctcc tggacttcac cgccagcctg gcccgcgcca gtgactcctc ttcctccagc 2340  
 tccctgggca gtggggaggc tgcggggctg ggacggggccc cctggaggat cccaccctcc 2400  
 gccccgcgc ccaagccag ccttgaccgc ctgatggggg ccttcgcctc cctggacctc 2460  
 aagagtcaga gaaaggagga gctgctggac tccaggactc cagccgggag aggggctggg 2520  
 acgtcggccc ggggacacca ctccgaccga gagccactgc tggggccccc tgcggcccg 2580  
 gccaggagcc tgctcctctt gccgttggag ggcaaggcca aacgcagcca ctccttcgac 2640  
 atgggggact ttgctgtgtc ggccggcgga ggggtcgtgc cgggcggcta cagtccctct 2700  
 cggaagggtc cgaacatctg gacgaagcgc agcctctctg tcaacggcat gctcttgccc 2760  
 tttgaggaga gtgacctgt gggggcccg gggacttttg gcagctccga atgggtgatg 2820  
 gagagcacgg tctaggtgg ggtgggcatg ctccctttcc tgtgcgcagg gtgggagaag 2880  
 gggaaagaat ctccactggca agtgtttgtg gagtttccat ggtgatgttt acatccaggg 2940  
 acagtttcgt ctccctgtca atggcctcgt gtccccccct acccgcaac acccatatca 3000  
 cctccccacc acccgccgg ggtgtgtcga gggaatgtgg actcgtcaa atgccggact 3060  
 gagcctgag tgtttggaaa ggcgagactc cgcctttcta atcacaatg tagcctacaa 3120  
 gcaagcggct ttggattgct tatg 3144

<210> 24  
 <211> 832  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser  
 1 5 10 15  
 Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg  
 20 25 30  
 Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu  
 35 40 45  
 Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys  
 50 55 60  
 Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu  
 65 70 75 80  
 Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg  
 85 90 95  
 Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg  
 100 105 110  
 Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg

115	120	125
Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser 130 135 140		
Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu 145 150 155 160		
Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn 165 170 175		
Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu 180 185 190		
Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro 195 200 205		
Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp 210 215 220		
His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln 225 230 235 240		
Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro 245 250 255		
Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr 260 265 270		
Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His 275 280 285		
Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp 290 295 300		
Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp 305 310 315 320		
His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln 325 330 335		
His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys 340 345 350		
Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro 355 360 365		
Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn 370 375 380		
Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe 385 390 395 400		
Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu 405 410 415		
Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr		

See  
DS  
Unit

420					425					430					
Ala	Pro	Pro	Lys	Ser	Arg	Leu	Ser	Asp	Ile	Thr	Gly	Ser	Ser	Lys	Thr
	435						440					445			
Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Ser	Pro
	450					455					460				
Pro	Glu	Arg	Ala	Val	Leu	Val	Ser	Glu	Val	Thr	Thr	Thr	Ser	Ala	Leu
465					470					475					480
Val	Lys	Trp	Ser	Val	Ser	Lys	Ser	Ala	Pro	Arg	Val	Lys	Met	Tyr	Gln
			485						490					495	
Leu	Gln	Tyr	Asn	Cys	Ser	Asp	Asp	Glu	Val	Leu	Ile	Tyr	Arg	Met	Ile
			500					505					510		
Pro	Ala	Ser	Asn	Lys	Ala	Phe	Val	Val	Asn	Asn	Leu	Val	Ser	Gly	Thr
	515					520						525			
Gly	Tyr	Asp	Leu	Cys	Val	Leu	Ala	Met	Trp	Asp	Asp	Thr	Ala	Thr	Thr
	530					535					540				
Leu	Thr	Ala	Thr	Asn	Ile	Val	Gly	Cys	Ala	Gln	Phe	Phe	Thr	Lys	Ala
545					550					555					560
Asp	Tyr	Pro	Gln	Cys	Gln	Ser	Met	His	Ser	Gln	Ile	Leu	Gly	Gly	Thr
			565						570					575	
Met	Ile	Leu	Val	Ile	Gly	Gly	Ile	Ile	Val	Ala	Thr	Leu	Leu	Val	Phe
			580					585					590		
Ile	Val	Ile	Leu	Met	Val	Arg	Tyr	Lys	Val	Cys	Asn	His	Glu	Ala	Pro
	595					600					605				
Ser	Lys	Met	Ala	Ala	Ala	Val	Ser	Asn	Val	Tyr	Ser	Gln	Thr	Asn	Gly
	610					615					620				
Ala	Gln	Pro	Pro	Pro	Pro	Ser	Ser	Ala	Pro	Ala	Gly	Ala	Pro	Pro	Gln
625					630					635					640
Gly	Pro	Pro	Lys	Val	Val	Val	Arg	Asn	Glu	Leu	Leu	Asp	Phe	Thr	Ala
			645						650					655	
Ser	Leu	Ala	Arg	Ala	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Gly
			660					665						670	
Gly	Glu	Ala	Ala	Gly	Leu	Gly	Arg	Ala	Pro	Trp	Arg	Ile	Pro	Pro	Ser
	675						680					685			
Ala	Pro	Arg	Pro	Lys	Pro	Ser	Leu	Asp	Arg	Leu	Met	Gly	Ala	Phe	Ala
	690					695					700				
Ser	Leu	Asp	Leu	Lys	Ser	Gln	Arg	Lys	Glu	Glu	Leu	Leu	Asp	Ser	Arg
705					710					715					720
Thr	Pro	Ala	Gly	Arg	Gly	Ala	Gly	Thr	Ser	Ala	Arg	Gly	His	His	Ser



<211> 183  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143  
Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys  
1 5 10 15  
Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg  
20 25 30  
Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys  
35 40 45  
Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly  
50 55 60  
Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn  
65 70 75 80  
Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala  
85 90 95  
Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln  
100 105 110  
Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu  
115 120 125  
Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg  
130 135 140  
Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160  
Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr  
165 170 175  
Tyr Ser Ser Thr Ala Leu Gln  
180

Sub  
DS  
cont